

SEQUENCE LISTING

<110> TEDESCO, Francesco
MARZARI, Roberto

<120> Antibodies anti C5 of the complement and their use

<130> 50294/016001

<150> PCT/EP2003/007487

<151> 2003-07-10

<150> MI2002A001527

<151> 2002-07-11

<160> 35

<170> PatentIn version 3.1

<210> 1

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(342)

<223> Light chain of the TS-A12/22 antibody

<400> 1

gac atc cgg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc	48
Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
1 5 10 15	

gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc	96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	

tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	

cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	

cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc	240
Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
65 70 75 80	

atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
85 90 95	

tat tat agt act cct cag ctc act ttc ggc gga agg acc aaa gtg gat	336
Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp	

100

105

110

atc aaa
Ile Lys

342

<210> 2
<211> 114
<212> PRT
<213> Homo sapiens

<400> 2

Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp
100 105 110

Ile Lys

<210> 3
<211> 345
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(345)
<223> Heavy chain of the TS-A12/22 antibody

<400> 3

cag gta cag ctg cag cag tca gag gga ggc gtg gtc cag cct ggg agg	48
Gln Val Gln Leu Gln Gln Ser Glu Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agt agc tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
ggc atg aac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt	144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
tca tac att agt agt agt agt agt acc ata tac tac gca gac tct gtg	192
Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val	
50 55 60	
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gcc gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aga ggg cct ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc	336
Ala Arg Gly Pro Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr	
100 105 110	
gtc tcc tca	345
Val Ser Ser	
115	

<210> 4
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 4

Gln Val Gln Leu Gln Gln Ser Glu Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val	
50 55 60	

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Pro Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

Val Ser Ser
115

<210> 5
<211> 750
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (750)
<223> scFv

<400> 5
gac atc cgg atg acc cag tct cca gac tcc ctg gct gtg tct ctg ggc 48
Asp Ile Arg Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt tta tac agc 96
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
tcc aac aat aag aac tac tta gct tgg tac cag cag aaa cca gga cag 144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
cct cct aag ctg ctc att tac tgg gca tct acc cgg gaa tcc ggg gtc 192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc act ctc acc 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
atc agc agc ctg cag gct gaa gat gtg gca gtt tat tac tgt cag caa 288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
tat tat agt act cct cag ctc act ttc ggc gga agg acc aaa gtg gat 336
Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp
100 105 110
atc aaa tcc gga ggg tcg acc ata act tcg tat aat gta tac tat acg 384

Ile	Lys	Ser	Gly	Gly	Ser	Thr	Ile	Thr	Ser	Tyr	Asn	Val	Tyr	Tyr	Thr		
	115						120					125					
aag	tta	tcc	tcg	agc	ggg	acc	cag	gta	cag	ctg	cag	cag	tca	gag	gga	432	
Lys	Leu	Ser	Ser	Ser	Gly	Thr	Gln	Val	Gln	Leu	Gln	Gln	Ser	Glu	Gly		
	130						135				140						
ggc	gtg	gtc	cag	cct	ggg	agg	tcc	ctg	aga	ctc	tcc	tgt	gca	gcg	tct	480	
Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser		
145					150					155					160		
gga	ttc	acc	ttc	agt	agc	tat	ggc	atg	aac	tgg	gtc	cgc	cag	gct	cca	528	
Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro		
				165					170					175			
ggg	aag	ggg	ctg	gag	tgg	gtt	tca	tac	att	agt	agt	agt	agt	agt	acc	576	
Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Tyr	Ile	Ser	Ser	Ser	Ser	Ser	Thr		
			180					185						190			
ata	tac	tac	gca	gac	tct	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	624	
Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp		
			195				200					205					
aat	tcc	aag	aac	acg	ctg	tat	ctg	caa	atg	aac	agc	ctg	aga	gcc	gag	672	
Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu		
	210					215				220							
gac	acg	gct	gtg	tat	tac	tgt	gcg	aga	ggg	cct	ggg	atg	gac	gtc	tgg	720	
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Gly	Met	Asp	Val	Trp		
225					230					235					240		
ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca							750	
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser								
				245					250								

<210> 6
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 6

Asp	Ile	Arg	Met	Thr	Gln	Ser	Pro	Asp	Ser	Leu	Ala	Val	Ser	Leu	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Ile	Asn	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser
			20					25					30		
Ser	Asn	Asn	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln
	35						40					45			
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
	50					55					60				

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Gln Leu Thr Phe Gly Gly Arg Thr Lys Val Asp
100 105 110

Ile Lys Ser Gly Gly Ser Thr Ile Thr Ser Tyr Asn Val Tyr Tyr Thr
115 120 125

Lys Leu Ser Ser Ser Gly Thr Gln Val Gln Leu Gln Gln Ser Glu Gly
130 135 140

Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
145 150 155 160

Gly Phe Thr Phe Ser Ser Tyr Gly Met Asn Trp Val Arg Gln Ala Pro
165 170 175

Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Ser Thr
180 185 190

Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
195 200 205

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
210 215 220

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro Gly Met Asp Val Trp
225 230 235 240

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
245 250

<210> 7
<211> 15
<212> DNA
<213> homo sapiens

<220>
<221> CDS

<222> (1)..(15)
<223> CDR1 region of VH

<400> 7
agc tat ggc atg aac 15
Ser Tyr Gly Met Asn
1 5

<210> 8
<211> 5
<212> PRT
<213> homo sapiens

<400> 8

Ser Tyr Gly Met Asn
1 5

<210> 9
<211> 51
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)..(51)
<223> CDR2 region of VH

<400> 9
tac att agt agt agt agt acc ata tac tac gca gac tct gtg aag 48
Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

ggc 51
Gly

<210> 10
<211> 17
<212> PRT
<213> homo sapiens

<400> 10

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 11
 <211> 18
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(18)
 <223> CDR3 region of VH

<400> 11
 ggg cct ggt atg gac gtc
 Gly Pro Gly Met Asp Val
 1 5

18

<210> 12
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 12
 Gly Pro Gly Met Asp Val
 1 5

<210> 13
 <211> 63
 <212> DNA
 <213> artificial sequence

<220>
 <223> linker

<220>
 <221> CDS
 <222> (1)..(63)
 <223> linker VL-VH

<400> 13
 tcc gga ggg tcg acc ata act tcg tat aat gta tac tat acg aag tta
 Ser Gly Gly Ser Thr Ile Thr Ser Tyr Asn Val Tyr Tyr Thr Lys Leu
 1 5 10 15

48

tcc tcg agc ggt acc
 Ser Ser Ser Gly Thr
 20

63

<210> 14
 <211> 21
 <212> PRT
 <213> artificial sequence

<220>

<223> linker

<400> 14

Ser Gly Gly Ser Thr Ile Thr Ser Tyr Asn Val Tyr Tyr Thr Lys Leu
1 5 10 15

Ser Ser Ser Gly Thr
20

<210> 15

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> Peptide comprising cleavage site of C5 convertase. Corresponding
to aa 727-744 of mature human protein (P01031).

<400> 15

Lys Asp Met Gln Leu Gly Arg Leu His Met Lys Thr Leu Leu Pro Val
1 5 10 15

Ser Lys

<210> 16

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(20)

<223> fibronectin derived peptide

<400> 16

Gly Glu Glu Ile Gln Ile Gly His Ile Pro Arg Glu Asp Val Asp Tyr
1 5 10 15

His Leu Tyr Pro
20

<210> 17

<211> 34

<212> DNA
<213> Artificial sequence /primer

<220>
<221> misc_feature
<222> (1)..(34)
<223> PCR primer

<400> 17
atccgagtcg acacctgtgg agagaaaggc aaag

34

<210> 18
<211> 34
<212> DNA
<213> Artificial sequence /primer

<220>
<221> misc_feature
<222> (1)..(34)
<223> PCR primer

<400> 18
tcctcagcgc gcggctctgg tggcagaccg aagg

34

<210> 19
<211> 33
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(33)
<223> Sequence derived from AF237583 GenBank acc. number

<400> 19
caggcggcgc gcgggcagcc ccaggaacca cag

33

<210> 20
<211> 94
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(94)
<223> Sequence derived from AF237583 GenBank acc. number

<400> 20
acgtcgatcg cctgctgaat tcttaagtac tatccaggcc cagcagtggg tttgggattg

60

gtttgccact agttttaccc ggggacaggg agag

94

<210> 21
<211> 41
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(41)
<223> Sequence derived from AF237583 GenBank acc. number

<400> 21
aggcggcgcg cgacaaaact cacacatgcc caccgtgccc a

41

<210> 22
<211> 33
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(33)
<223> Sequence derived from J00220 GenBank acc. number

<400> 22
caggcggcgc gcgttcacct aactccacct acc

33

<210> 23
<211> 32
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(32)
<223> Sequence derived from J00220 GenBank acc. number

<400> 23
ccgtactag ttttaccgcg caagcggtcg at

32

<210> 24
<211> 31
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(31)
<223> Sequence derived from L27437 GenBank acc. number

<400> 24
caggcggcgc gcggcagacc gaaggctcca c 31

<210> 25
<211> 32
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(32)
<223> Sequence derived from J00220 GenBank acc. number

<400> 25
ccgctactag ttttaccagg agagtgggag ag 32

<210> 26
<211> 36
<212> DNA
<213> Mus musculus

<220>
<221> misc_feature
<222> (1)..(36)
<223> Sequence derived from L27437 GenBank acc. number

<400> 26
caggcggcgc gcggttgtaa gccttgcata tgtaca 36

<210> 27
<211> 33
<212> DNA
<213> Rattus norvegicus

<220>
<221> misc_feature
<222> (1)..(33)
<223> Sequence derived from M28671 GenBank acc. number

<400> 27
caggcggcgc gcgggctagt cagaaaacca cag 33

<210> 28
<211> 33
<212> DNA
<213> Rattus norvegicus

<220>

<221> misc_feature
<222> (1)..(33)
<223> Sequence derived from M28671 GenBank acc. number

<400> 28
ccgtactag ttttaccgg aggccgggag atg 33

<210> 29
<211> 33
<212> DNA
<213> Rattus norvegicus

<220>
<221> misc_feature
<222> (1)..(33)
<223> Sequence derived from M28671 GenBank acc. number

<400> 29
caggcggcgc gccacaaatg ccctacatgc cct 33

<210> 30
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(35)
<223> Universal oligonucleotide for VL1 amplification.

<400> 30
caggtgtgca ctccgacatc crgdtgaccc agtct 35

<210> 31
<211> 35
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(35)
<223> nucleotide in position 29 is "n"
Universal oligonucleotide for VL2 amplification.

<400> 31
caggtgtgca ctccgatatt gtgwtgacac agwct 35

<210> 32
<211> 31

<212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)..(31)
 <223> Universal oligonucleotide for VL3 amplification.

 <400> 32
 caggtgtgca ctcgcagcct gtgctgcary c 31

 <210> 33
 <211> 35
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)..(35)
 <223> Universal oligonucleotide for VL4 amplification.

 <400> 33
 caggtgtgca ctcgtcctat gwgctgacwc agcca 35

 <210> 34
 <211> 29
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)..(29)
 <223> Universal oligonucleotide for JH1 amplification.

 <400> 34
 gaccgcgcgc cggagacrgt gaccagggt 29

 <210> 35
 <211> 29
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)..(29)
 <223> Universal oligonucleotide for JH2 amplification.

 <400> 35
 gaccgcgcgc cagagacggt gaccrtkgt 29